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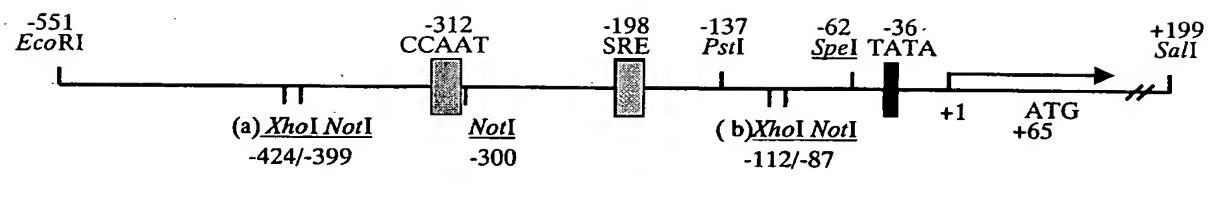
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Fig.1

1 GAATTCAATGG TGTTTTGATC ATTTTAAATT TTTATATGGC GGGTGGTGGG CAACTCGCTT 60  
60 CCGGGCAACT CGCTTACCGA TTACGTTAGG GCTGATATTT ACGTAAAAAT CGTCAAGGGA 120  
121 TGCAAGACCA AAGTAGTAAA ACCCCGGAGT CAACAGCATC CAAGCCCAAG TCCTTCACGG 180  
181 AGAAACCCCA GCGTCCACAT CACGAGCGAA GGACCACCTC TAGGCATCGG ACGCACCATC 240  
241 CAATTAGAAG CAGCAAAGCG AAACAGCCC AGAAAAAGGT CGGCCCGTCG GCCTTTCTG 300  
301 CAACGCTGAT CACGGGCAGC GATCCAACCA ACACCCCTCCA GAGTGACTAG GGGCGGAAAT 360  
361 TTAAAGGGAT TAATTTCCAC TCAACCACAA ATCACAGTCTG TCCCCGGTAT TGTCCTGCAG 420  
421 AATGCAATTG AAACTCTTCT GCGAATCGCT TGGATTCCCC GCCCCTGGCC GTAGAGCTTA 480  
481 AAGTATGTCC CTTGTCGATG CGATGTATCA CAACATATAA ATACTAGCAA GGGATGCCAT 540  
541 GCTTGGAGGA TAGCAACCGA CAACATCACA TCAAGCTCTC CCTTCTCTGA ACAATAAAC 600  
601 CCACAGAAGG CATT 615

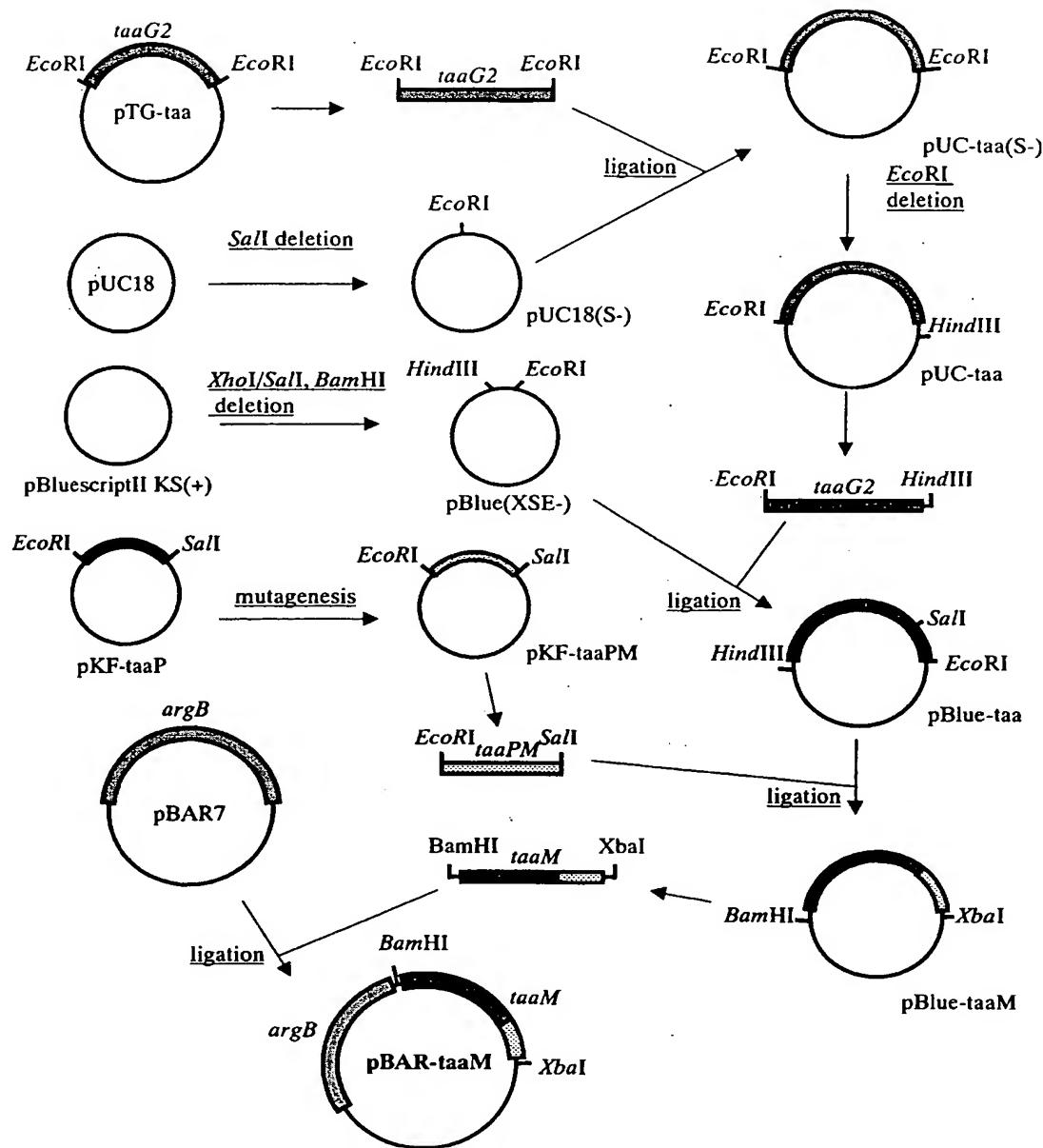
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Fig.2



- [diagonal line box]: CCAAT sequence (binding factor of a wide domain transcription activation factor (HAP complex))
- [vertical line box]: SRE(binding factor of a transcription activation factor of a starch degrading enzyme gene cluster (AmyR))
- [solid black box]: TATA-box
- +1: transcription initiation site

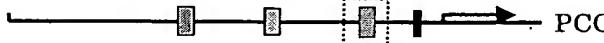
Fig.3



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Fig.4

	Amylase Activity (U/g dry mycelia)	(ratio)
 taaP	1041	1
 PCCAATb	786	0.8
 PSREb	1319	1.3
 PCSP	4269	4.1

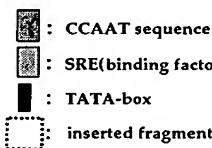
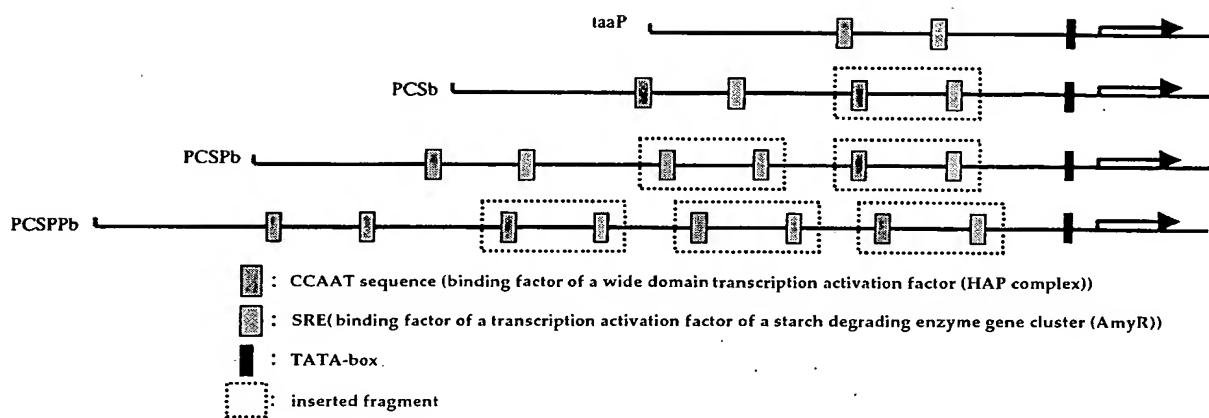
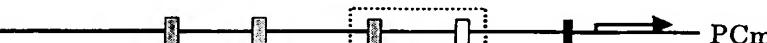
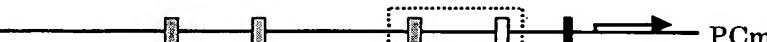
  
■ : CCAAT sequence (binding factor of a wide domain transcription activation factor (HAP complex))  
■ : SRE(binding factor of a transcription activation factor of a starch degrading enzyme gene cluster (AmyR))  
■ : TATA-box  
□ : inserted fragment

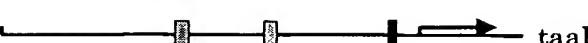
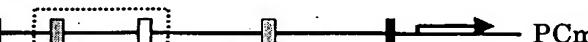
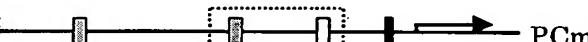
Fig.5



Promoter	Amylase Activity			
	Starch		Glucose	
	(U/g dry mycelia)	(ratio)	(U/g dry mycelia)	(ratio)
taaP	916	1	25	1
PCSB	4601	5.0	601	24.1
PCSPb	6455	7.0	740	29.6
PCSPPb	7084	7.7	941	37.7

Fig. 6

	Amylase Activity (U/g dry mycelia)	(ratio)
 taaP	1041	1
 PCmSa	2178	2.1
 PCmSN	1047	1.0
 PCmSb	3237	3.2
 PCmSS	2130	2.0

 : CCAAT sequence (binding factor of a wide domain transcription activation factor (HAP complex))  
 : SRE (binding factor of a transcription activation factor of a starch degrading enzyme gene cluster (AmyR))  
 : modified SRE  
 : TATA-box  
 : inserted fragment

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Fig. 7

Strain	Copy Number	Amount of Amylase	
		(g/L)	(ratio)
ABPU1	0	0.01	
taa2	1	0.29	1
CSb17	1	1.46	5.0
CSb16	multiple	9.90	34.1
CSP6	multiple	6.41	22.1
CSPb19	multiple	7.35	25.3

ABPU1 ; host      taa2 ; wild type promoter

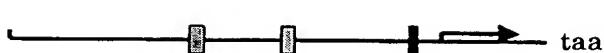
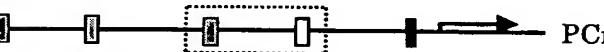
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Fig. 8

Strain	Amount of Amylase (g/L)		
	SPY medium	MPY medium	GPY medium
CSP6	6.41	4.86	2.94
CSPb19	7.35	5.25	6.25

The production amount of amylase is shown as a conversion value as compared with the specific activity of Taka-amylase is 100 U/mg.

Fig. 9

	Amylase Activity (U/g dry mycelia)	(ratio)
	1041	1
	3237	3.2
	1634	1.6

-  : CCAAT sequence (binding factor of a wide domain transcription activation factor (HAP complex))
-  : SRE(binding factor of a transcription activation factor of a starch degrading enzyme gene cluster (AmyR))
-  : modified SRE
-  : TATA-box
-  : inserted fragment

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Fig. 1 0

The diagram shows a horizontal line representing the SRE sequence. Three black boxes are positioned along the line, with a dotted arrow pointing from the first two boxes to the sequence below. A third black box is located further down the line. An arrow points to the right from the third box.

SRE sequence		Amylase Activity (U/g dry mycelia) (ratio)	
CGGAAATTAAAGG	taaP	1041	1
CGGAAATT <u>A</u> CGG	taaS	1209	1.2
CGGAAATT <u>A</u> TTA	MSRE2	792	0.8

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Fig. 1 1

Promoter	Amylase Activity			
	<i>A. oryzae</i> KBN616		<i>A. oryzae</i> KBN6217	
	(U/g mycelia)	(ratio)	(U/g mycelia)	(ratio)
non-recombinant strain	377	1	13003	1
PCSPb	21702	57.6	137179	10.6

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Fig. 1 2

Promoter	Laccase Activity	
	( $\Delta$ O.D. / 0.1ml)	(ratio)
non-recombinant strain	0	-
taaP	174	1
PCSPb	136	0.8
PCSPPb	281	1.6

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